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              GenCore version 4.5
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OM protein - protein search, using sw model

Run on:      May 7, 2002, 12:01:59 ; Search time 32.09 Seconds
                                        (without alignments)
                                     337.077 Million cell updates/sec

Title:          US-09-772-103-10
Perfect score:  742
Sequence:     1 MAVLVLFLCLVAFPSCVLSQ..........MKRGYAMDYWGQGTLVTVSS 142

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Database :

Searched:       219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:       219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_68:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	588.5	79.3	141	2	S52446	Ig heavy chain v r
2	561.5	75.7	139	2	A32456	Ig heavy chain pre
3	558	75.2	140	2	S55028	Ig heavy chain v r
4	528.5	71.2	135	2	S31913	Ig gamma-2A chain
5	525	70.8	117	2	S10111	Ig heavy chain v r
6	510	68.7	140	2	S14238	Ig heavy chain v r
7	506	68.2	144	1	G2MS14	Ig gamma-1 chain p
8	504.5	68.0	144	2	S11244	Ig gamma-2a chain
9	491	66.2	140	2	I37782	Ig heavy chain pre
10	483.5	65.2	137	2	S31676	Ig variable region
11	481.5	64.9	120	2	PL0087	Ig heavy chain v r
12	481.5	64.9	139	2	S31586	Ig heavy chain v r
13	478	64.4	116	2	A33932	Ig heavy chain v r
14	478	64.4	155	2	S31511	Ig mu chain precur
15	476	64.2	147	2	S13519	Ig heavy chain - h
16	475	64.0	116	1	GIMS10	Ig heavy chain v r
17	475	64.0	155	2	S31512	Ig heavy chain pre
18	469	63.2	112	2	S11100	Ig heavy chain - h
19	467.5	63.0	145	2	S78055	Ig heavy chain v r
20	467	62.9	130	2	S31690	Ig heavy chain pre
21	466	62.8	114	2	S11106	Ig heavy chain v r
22	464	62.5	113	2	S11101	Ig heavy chain v r
23	464	62.5	115	1	HVMS14	Ig heavy chain v r
24	464	62.5	116	2	S11102	Ig heavy chain v r
25	464	62.5	127	2	B31807	Ig heavy chain pre
26	459	61.9	146	2	S09711	Ig heavy chain v r
27	458	61.7	118	2	PQ0266	Ig heavy chain v r
28	456.5	61.5	117	2	S38563	Ig heavy chain v r
29	456	61.5	146	2	S09710	Ig heavy chain v r
30	454	61.2	139	2	S31696	Ig heavy chain v r
31	453	61.1	140	2	A49045	Ig heavy chain v r
32	450.5	60.7	116	2	S42484	Ig heavy chain v r
33	449	60.5	114	2	S11099	Ig heavy chain v r
34	449	60.5	115	2	S11103	Ig heavy chain v r
35	447	60.2	106	2	S26322	Ig heavy chain v r
36	447	60.2	112	2	S11108	Ig heavy chain v r
37	446	60.1	135	2	S78051	Ig heavy chain pre
38	444.5	59.9	118	2	S32786	Ig heavy chain (an
39	444	59.8	121	2	S33131	Ig heavy chain v r
40	442.5	59.6	140	2	S78052	Ig heavy chain pre
41	441	59.4	114	2	S26321	Ig mu heavy chain
42	441	59.4	140	2	S54239	Ig heavy chain v r
43	441	59.4	144	2	S54244	Ig mu heavy chain
44	439	59.2	121	2	D30560	Ig heavy chain V r
45	438.5	59.1	141	2	S54236	Ig mu heavy chain

ALIGNMENTS

```
RESULT   1
S52446
Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 03-Aug-1995 #text_change 23-Jul-1999
C;Accession: S52446
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged
A;Reference number: S52445
A;Accession: S52446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <BER>
A;Cross-references: EMBL:X82692; NID:g673441; PIDN:CAA58013.1; PID:g673442
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match             79.3%;  Score 588.5;  DB 2;  Length 141;
Best Local Similarity   81.0%;  Pred. No. 7e-45;
Matches  115;  Conservative   12;  Mismatches   14;  Indels    1;  Gaps    1;

Qy    1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPP 60
        ||||||||||||||||||||| ||||||||||| |||||||||||||||||||||||||||
Db    1 MAVLVLFLCLVAFPSCVLSQVQLKESGPGLVAPSQSLSITCTVSGFSLTSYGVHWVRQPP 60

Qy   61 GKGLEWLGVIWAGGTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPH 120
        ||||| |||||||||  ||||||||||| |||||:|||||| |||:| |||||||||   |
Db   61 GKGLEGLGVIWAGGSTNYNSALMSRLSISKDNSKSQVFLKMNSLQIDDTAMYYCARSPT- 119

Qy  121 AMKRGYAMDYWGQGTLVTVSS 142
         : ||||||||||||| |||||
Db  120 STMDTPYAMDYWGQGTSVTVSS 141


RESULT   2
A32456
Ig heavy chain precursor V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C;Accession: A32456
R;Dombrink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.
J. Biol. Chem. 264, 4513-4522, 1989
A;Title: Variable region primary structures of a high affinity anti-fluorescein immun
A;Reference number: A32456; MUID:89174706
A;Accession: A32456
A;Status: preliminary
A;Molecule type: mRNA
```

A;Residues: 1-139 <DOM>
A;Cross-references: GB:J04609; NID:g556316; PIDN:AAA50298.1; PID:g556317
A;Note: the authors translated the codon CAC for residue 20 as Gln, and CAC for residue
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match   75.7%; Score 561.5; DB 2; Length 139;
Best Local Similarity   76.4%; Pred. No. 1.6e-42;
Matches 110; Conservative 14; Mismatches 13; Indels   7; Gaps   2;

Qy   1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPP 60
          ||||||||||||||||||||| | :||:||||||||||||||||:|:||:||:||||
Db   1 MAVLVLFCLVTFPSCVLSHVHLKESGPVLVAPSQSLSITCTVSGFSLTNYGVHWVRQPP 60

Qy   61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPH 120
          ||||||||||||||||| ||||||:|| |||::| :||::| |||||||
Db   61 GKGLEWLGVIWAGGNTNYNSALMSRLSISKDNSKSQVFLKMNSLQIDDTAIYYCAK---- 116

Qy 121 AMMKR--GYAMDYWGQGTLVTVSS 142
          :|| |||||||||||||
Db 117 -RLERIFYYAMDYWGQGTSVTVSS 139

RESULT 3
S55028
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
C;Accession: S55028
R;Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolies, M.N.; Sheriff,
J. Mol. Biol. 248, 344-360, 1995
A;Title: Structure and specificity of the anti-digoxin antibody 40-50.
A;Reference number: S55027; MUID:95257394
A;Accession: S55028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <JEF>
A;Cross-references: EMBL:L31403; NID:g476717; PIDN:AAA38191.1; PID:g476718
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match   75.2%; Score 558.; DB 2; Length 140;
Best Local Similarity   76.1%; Pred. No. 3.3e-42;
Matches 108; Conservative 15; Mismatches 17; Indels   2; Gaps   1;

Qy   1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPP 60
          |||||||||||||||||| :|||:||||||||||||||||:|:|||:||||||
Db   1 MAVLVLFLCLVAFPSCVLSQVHLKESGPGLVAPSQSLSITCTVSGFSLTTYGVHWFRQPP 60

Qy   61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPH 120
          ||||||||||||||||| ||||||:|| |||::|| |:::| ||||||||
Db   61 GKGLEWLGLIWAGGNTDYNSALMSRLSINKSKSQVFLKMNSLQADDTAMYYCARF--R 118

Qy 121 AMMKRGYAMDYWGQGTLVTVSS 142
          :|||||||||||||||
Db 119 FASYYDYAVDYWGQGTSVTVSS 140

RESULT 4
S31913
Ig gamma-2A chain precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 23-Jul-1999
C;Accession: S31913
R;Bespalov, I.A.; Hiyanov, P.A.; Lukashevich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponova
submitted to the EMBL Data Library, January 1993
A;Reference number: S31913
A;Accession: S31913
A;Molecule type: mRNA

A;Residues: 1-135 <BES>
A;Cross-references: EMBL:X70822; NID:g57921; PIDN:CAA50153.1; PID:g57922
A;Experimental source: strain BALB/c
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-11/Domain: signal sequence #status predicted <SIG>
F;12-135/Product: Ig gamma-2A chain (fragment) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match   71.2%; Score 528.5; DB 2; Length 135;
Best Local Similarity   70.4%; Pred. No. 1.2e-39;
Matches 100; Conservative 19; Mismatches 16; Indels   7; Gaps   1;

Qy   1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPP 60
          ||| | ||:||||||||| :||:| :|||||||||||||:|:||||:|||||
Db   1 MAVLGLLFCLVTFPSCVLSQVLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSP 60

Qy   61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPH 120
          |||||||||||||||||| ||:|:||: :|||::| :||::||:||||||
Db   61 GKGLEWLGVIWSGGSTDYNAAFISRLSISKDNSKSQVFFKMNSLQANDTAIYYCAR---- 116

Qy 121 AMMKRGYAMDYWGQGTLVTVSS 142
          |:| |||||||||||
Db 117 ---ELVYYFDYWGQGTTLTVSS 135

RESULT 5
S10111
Ig heavy chain V region (clone 26) precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S10111
R;Kaartinen, M.; Solin, M.L.; Maekelae, O.
EMBO J. 8, 1743-1748, 1989
A;Title: 'Allelic' forms of immunoglobulin V genes in different strains of mice.
A;Reference number: S10111; MUID:89356648
A;Accession: S10111
A;Molecule type: mRNA
A;Residues: 1-117 <KAA>
A;Cross-references: EMBL:X15471; NID:g50005; PIDN:CAA33499.1; PID:g50006
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match   70.8%; Score 525.; DB 2; Length 117;
Best Local Similarity   85.3%; Pred. No. 2.2e-39;
Matches 99; Conservative 11; Mismatches   6; Indels   0; Gaps   0;

Qy   1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPP 60
          |||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db   1 MAVLVLFLCLVAFPSCVLSQVQLKESGPGLVAPSQSLSITCTVSGFSLTSYGVHWVRQPP 60

Qy   61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCAR 116
          ||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db   61 GKGLEWLGVIWAGGSTNYNSALMSRLSISKDNSKSQVFLKMNSLQTDDTAMYYCAR 116

RESULT 6
S14238
Ig gamma-1 chain precursor (15C5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S14238
R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclonal antibod
A;Reference number: S14236; MUID:91006173
A;Accession: S14238
A;Molecule type: mRNA
A;Residues: 1-140 <VAN>
A;Cross-references: EMBL:X56392; NID:g51619; PIDN:CAA39803.1; PID:g747853

C;Superfamily: immunoglobulin; immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;26-108/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity   68.7%;   Score 510;   DB 2;   Length 140;
Matches   94;   Conservative   21;   Mismatches   13;   Indels   6;   Gaps   1;

Qy   9 CLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYVWRQPPGKGLEWLG
         |||||||||||||||||:||||:|||:|||||||||||||:||||||:||||||||||||
Db   1 CLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTTYGVHWIRQSPGKGLEWLG   60

Qy   69 VIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPHAMMKRGYA 128
         |||:|:||:||:||:|:|||||||||||||||||||||||||||||||| ::| ||||||
Db   61 VIWSGGSTDYNAAFISRLSINKDNSKSQVFFKMNSLQANDTAIYYCARN-----YWGTS 114

Qy   129 MDYWGQGTLVTVSS 142
         ||||||||||||||
Db   115 MDYWGQGTSVTVSS 128

RESULT   7
G2MS14
Ig heavy chain precursor V region (MOPC 141) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 16-Jun-2000
C;Accession: A02094
R;Sakano, H.; Maki, R.; Kurosawa, Y.; Roeder, W.; Tonegawa, S.
Nature 286, 676-683, 1980
A;Title: Two types of somatic recombination are necessary for the generation of complete
A;Reference number: A93229; MUID:81012133
A;Accession: A02094
A;Molecule type: DNA
A;Residues: 1-144 <SAK>
A;Cross-references: GB:V00768; GB:J00491; NID:g51615; PIDN:CAA24149.1; PID:g51616
A;Note: the sequence shown was determined from a differentiated gene isolated from a mye
A;Note: the authors translated the codon TAT for residue 51 as Thr and TTA for residue g
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin; immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Product: signal sequence #status predicted <SIG>
F;20-144/Product: Ig heavy chain V region (MOPC 141) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM> #status predicted

Query Match
Best Local Similarity   68.2%;   Score 506;   DB 1;   Length 144;
Matches   97;   Conservative   15;   Mismatches   30;   Indels   2;   Gaps   1;

Qy   1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYVWRQPP   60
         |||| || |||||||||||||||||||||||||||:|||:|||||||||| |||||||||
Db   1 MAVLALLFCLATFPSCILSQVQLKESGPGLVAPSQSLSITCTVSGFSLTGYGVNWVRQPP   60

Qy   61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGP-- 118
         |||||||||||:|:||:||:||:|:|||||||||:||:: |||||||||||||||||
Db   61 GKGLEWLGTIWGNGSTDYNSTLKSRLTITTKDNSKSQVFLKMNSLQTDDTARYYCASVSIY 120

Qy   119 PHAMMKRGYAMDYWGQGTLVTVSS 142
         : : :|||||||||||||||
Db   121 YYGRSDKYFTLDYWGQGTSVTVSS 144

RESULT   8
S11244
Ig gamma-2a chain precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S11244
R;Wellman, A.A.; Meares, C.F.
Nucleic Acids Res. 18, 5281, 1990
A;Title: Sequences of the Lym-1 antibody heavy and light chain variable regions.

A;Reference number: S11244; MUID:90384832
A;Accession: S11244
A;Molecule type: mRNA
A;Cross-references: EMBL:X53483
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity   68.0%;   Score 504.5;   DB 2;   Length 144;
Matches 100;   Conservative   15;   Mismatches   22;   Indels   5;   Gaps   2;

Qy   1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYVWRQPP   60
         ||| :||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MAVLGLLLCLVTFPSCVLSQVQLKESGPGLVAPSQSLSITCISGFSLTSYGVHWVRQPP   60

Qy   61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPH 120
         ||| :||| |: || ||:|||||:|||:| ||:::|| |:::||||||||||||||||||
Db   61 GKGLEWLVIWSDGSTTYNSALKSRLSISKDNSKSQVFLKMNSLQTDDTAIYYCA---SH 117

Qy   121 AMMKRGYAMDYWGQGTLVTVSS 142
         :| |||||||||||||
Db   118 YGSTLAFAS--WGHGTLVTVSA 137

RESULT   9
I37782
Ig variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: I37782; S25476
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed b
A;Reference number: A36876; MUID:94119917
A;Accession: I37782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <RES>
A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity   66.2%;   Score 491;   DB 2;   Length 140;
Matches 102;   Conservative   11;   Mismatches   27;   Indels   2;   Gaps   1;

Qy   1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYVWRQPP   60
         | || || | | |||||||||||||||||||||||||:|||:||||||||||||||||||
Db   1 MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPP   60

Qy   61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPH 120
         |||||||| |: | || ::|| ||:|||||||| || :|||||||||||||||||||||
Db   61 GKGLEWIGYIYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHNSS 120

Qy   121 AMMKRGYAMDYWGQGTLVTVSS 142
         :| |||||||||||||
Db   121 SWYGRYF--DYWGQGTLVTVSS 140

RESULT 10
S31676
Ig heavy chain v region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from t
A;Reference number: S31585

```
A;Accession: S31676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match             65.2%;  Score 483.5;  DB 2;  Length 137;
Best Local Similarity   71.1%;  Pred. No. 1.1e-35;
Matches  101;  Conservative  11;  Mismatches  25;  Indels  5;  Gaps  2;

Qy     1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPP 60
           | | |||| |||||||||||||||||||||||||||||: :|| |:|||
Db     1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPA 60

Qy    61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPH 120
           |||||: |: :|||| :| :||| |||||||||||| ||||||||||||||||
Db    61 GKGLEWIGRIYTSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDAP- 119

Qy   121 AMMKRGYAMDYWGQGTLVTVSS 142
           :| : | ||  |||||
Db   120 -LM--YGMDVWGQGTTVTVSS 137

RESULT 11
PL0087
Ig heavy chain V region (E3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0087
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248
A;Accession: PL0087
A;Molecule type: mRNA
A;Residues: 1-120 <MEE>
A;Cross-references: GB:X58593; GB:Y00794; NID:g51571; PIDN:CAA41468.1; PID:g938252
A;Experimental source: strain BALB/c
A;Note: the sequence shown here is from the VH region of an antiidiotypic monoclonal ant
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match             64.9%;  Score 481.5;  DB 2;  Length 120;
Best Local Similarity   75.6%;  Pred. No. 1.5e-35;
Matches  93;  Conservative  12;  Mismatches  15;  Indels  3;  Gaps  1;

Qy    20 QVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPPGKGLEWLGVIWAGGTTNYN 79
          |||| |||||: :|||||||||||||||||||||||||||||: |||||||||||||||:|||
Db     1 QVQLKRSGPGLVAPSQSLSITCTVSGVHWVRQPPGKGLEWLGVIWAGGSTNYN 60

Qy    80 SALMSRLTISKDNQVSLKLSSVTAADTAVYYCARGPPHAMMKRGYAMDYWGQGTLVT 139
          :||||||||||||| |||:: :|||||||||||||||| : |||||||||||
Db    61 SALMSRLTISKDNSKSQVFLKMTSLQIDDTAMYYCAR--DSHCCQAYGMDYWGQGTSVT 117

Qy   140 VSS 142
          |||
Db   118 VSS 120

RESULT 12
S31586
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R;Accession: S31586
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
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A;Description: Mechanisms that generate human immunoglobulin diversity operate from t
A;Reference number: S31585
A;Accession: S31586
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
A;Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match             64.9%;  Score 481.5;  DB 2;  Length 139;
Best Local Similarity   71.1%;  Pred. No. 1.7e-35;
Matches  101;  Conservative  13;  Mismatches  25;  Indels  3;  Gaps  2;

Qy     1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPP 60
           | | |||| ||||||||||||||||||||||||||||||||: :|| |:|||
Db     1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPA 60

Qy    61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPH 120
           |||||: |: :|||| :| :||| |||||||||||||| ||||||||||||||| :|
Db    61 GKGLEWIGRIYTSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARG--G 118

Qy   121 AMMKRGYAMDYWGQGTLVTVSS 142
           :|| : | ||   |||||
Db   119 LGIRRG-AFDIWGQGTMVTVSS 139

RESULT 13
A33932
Ig mu chain precursor V region (D23) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 23-May-1997
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated ger
A;Reference number: A33932; MUID:89282823
A;Accession: A33932
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <BAC>
A;Cross-references: GB:M27107
A;Note: the authors translated the codon CTA for residue 18 as Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match             64.4%;  Score 478;  DB 2;  Length 116;
Best Local Similarity   75.9%;  Pred. No. 2.9e-35;
Matches  88;  Conservative  17;  Mismatches  11;  Indels  0;  Gaps  0;

Qy     1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPP 60
           |||||||||||||||||||||||||||||||||||||||||: |
Db     1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSP 60

Qy    61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCAR 116
           ||||||||||||||||: |||||||||||| :|:|||: ||||
Db    61 GKGLEWLGVIWSGGSTDYNAAFISRLSISKDNSKSQVFFKMNSLQANDTAIYYCAR 116

RESULT 14
S31511
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA a
A;Reference number: S31509
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A;Accession: S31511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match   64.4%;   Score 478; DB 2;   Length 155;
Best Local Similarity 69.7%; Pred. No. 3.9e-35;
Matches   99; Conservative   10; Mismatches   33; Indels   0; Gaps   0;

Qy   1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGYYWVRQPP 60
         | | || || | ||||||||||||||||||||||||||: |||| :|: || : ||||
Db   14 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPP 73

Qy   61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQYSLKLSSVTAADTAVYYCARGPPH 120
         ||||||:| : |: :| : | : || ||||||| ||| :|||||||||||||||||||
Db   74 GKGLEWIGIYITGSATYNPPLKSRVTISVDTSKNQFSLKVSSVTAADTAVYYCARGGGI 133

Qy 121 AMMKRGYAMDYWGQGTLVTVSS 142
         : || ||||| |||||
Db 134 SSWYDYYGMDVWGQGTTVTVSS 155

RESULT 15
S13519
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with x-linked
A;Reference number: S13519; MUID:91187691
A;Accession: S13519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match   64.2%;   Score 476; DB 2;   Length 147;
Best Local Similarity 69.4%; Pred. No. 5.5e-35;
Matches 100; Conservative   12; Mismatches   26; Indels   6; Gaps   2;

Qy   1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGYY--WVRQ 58
         | | || || | ||||||||||||||||||||||||||: |||| :|: || ||
Db   8 MKHLWFFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGGSISSYYWGWIRQ 67

Qy   59 PPGKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGP 118
         ||||||||:| : |: :| : | : || ||||||| |||: |||||||||||||||||||
Db   68 PPGKGLEWIGSIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-- 125

Qy 119 PHAMMKRGYAMDYWGQGTLVTVSS 142
         :: | || ||||| |||||
Db 126 --PLLWFGELFDYWGQGTLVTVSS 147